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APRUCATION NO 19 DE FILING PATE / 19 OHSUFE NAMED INVENTOR

O21839

BURNS DOANE SWECKER & MATHIS L L F

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ALEXANDRIA VA 22313-1404

DATE MAILED:

ATTORNEY DOCKET NO.

EXAMINER
SLOBODY ANSKY, E

ART UNIT PAPER NUMBER

03/23/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



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SERIAL NUMBER	FILING DATE		FIRST N	AMED APPLICANT	ATTORNEY DOCKET NO.
		1			
					EXAMINER
				ARTUNIT	DADED NUMBER
				ART UNIT	PAPER NUMBER
				1652	6

Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

Any inquiry concerning this communication should be directed to Examiner Elizabeth Slobodyansky, Art Unit 1652, whose telephone number is (703) 306-3222.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

APPLICANT IS GIVEN A ONE MONTH EXTENDABLE PERIOD WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Elizabeth Slobodyansky, PhD

Primary Examiner Art Unit 1652

L



NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

 2. This application does not contain, as a separate part of the disclosure on paper copy, a Listing" as required by 37 C.F.R. 1.821(c). 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as 37 C.F.R. 1.821(e). 4. A copy of the "Sequence Listing" in computer readable form has been submitted. How content of the computer readable form does not comply with the requirements of 37 C. and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing" 	s required by vever, the .F.R. 1.822
 37 C.F.R. 1.821(e). 4. A copy of the "Sequence Listing" in computer readable form has been submitted. How content of the computer readable form does not comply with the requirements of 37 C. 	vever, the .F.R. 1.822
content of the computer readable form does not comply with the requirements of 37 C.	.F.R. 1.822
	ting."
5. The computer readable form that has been filed with this application has been found to and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Subscomputer readable form must be submitted as required by 37 C.F.R. 1.825(d).	
6. The paper copy of the "Sequence Listing" is not the same as the computer readable from "Sequence Listing" as required by 37 C.F.R. 1.821(e).	om of the
7. Other:	
Applicant Must Provide:	
An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".	
An <u>initial</u> or substitute paper copy of the "Sequence Listing", as well as an amendment dir into the specification.	recting its entr
A statement that the content of the paper and computer readable copies are the same an applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(1.825(b) or 1.825(d).	
For questions regarding compliance to these requirements, please contact:	
For Rules Interpretation, call (703) 308-4216 For CRF Submission Help, call (703) 308-4212 PatentIn Software Program Support (SIRA) Technical Assistance	

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

ERROR DETECTED SUGGESTED CORRECTION

13 ____ Patentin ver. 2.0 "bug"

	ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/402, 093	
ATTNI	NEW DILLES CASES: PL	EASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE	
1	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line.	
·—	TTTOPPOS TTOOLOGO	This may occur if your file was retrieved in a word processor after creating it.	
		Please adjust your right margin to .3, as this will prevent "wrapping".	_
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line.	H H
	···appoor	This may occur if your file was retrieved in a word processor after creating it.	S
		Please adjust your right margin to .3, as this will prevent "wrapping".	-
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	AVAILABLE
4	Misaligned Amino Acid	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs	=
` 	Numbering	between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	₽B
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.	
		Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	m
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue.	\aleph
	· · · · · · · · · · · · · · · · · · ·	As per the rules, each n or Xáa can only represent a single residue.	$\stackrel{\scriptscriptstyle{\leftarrow}}{\prec}$
		Please present the maximum number of each residue having variable length and	そ
•		indicate in the (ix) feature section that some may be missing.	•
7	Patentin ver. 2.0 "bug"	A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid	
		sequence(s) Normally, Patentin would automatically generate this section from the	
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section	
		to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>	
		sections for Artificial or Unknown sequences.	
8 8	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence:	
	(OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X:	:"1
		(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS"	,
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped	
	•	Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence.	
	(NEW RULES)	<210> sequence id number	
		\$400> sequence id number	
		000	
0	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence Listing.	
	(NEW RULES)	Use of <220> to <223> is MANDATORY if n's or Xaa's are present.	
		In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
i	Use of <213>Organism	Sequence(s) are missing this mandatory field or its response.	
1	(NEW RULES)	//	
J	-	T	
2	Use of <220>Feature	Sequence(s) are missing the <220>Feature and associated headings.	
	(NEW RULES)	Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section.	
•		(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new R	≀uies)
		Toda I contain togetter, ordinal, tak out the interpretation of the containing	

Instead, please use "File Manager" or any other means to copy file to floppy disk.

Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted

file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).

Does Not Comply

Corrected Diskette Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/402,093

DATE: 03/22/2001 TIME: 09:36:28

input Set : A:\F962 SEQUENCE.txt

Output Set: N:\CRF3\03222001\I402093.raw

3 <110> APPLICANT: Suntory Limited

5 < 120 > TITLE OF INVENTION: Process for producing peptides using a

helper peptide

8 <130> FILE REFERENCE: F962

0 10 (140) CURRENT APPLICATION NUMBER: US/09/402,093 10 (141) CURRENT FILING DATE: 1999-09-29

 $10\ <\!150\!>$ PRTOR APPLICATION NUMBER: JP $10\!-\!032272$

11 <151> PRIOR FILING DATE: 1998-01-30

13 <160> NUMBER OF SEQ ID NOS: 24

ERRORED SEQUENCES

424 <210> SEQ ID NO: 24

425 <211> LENGTH; 5

426 <212> TYPE: PRT

427 <213> ORGANISM: Artificial Sequence

429 <220> FEATURE:

430 <223> OTHER INFORMATION: Amino acid sequence containing a site cleaved by

431 Kex2 Protease

433 <400> SEQUENCE: 24

434 Ser Cys His Lys Arg

135

E--> 436(?? - 10/13 -E--> 444

E--> 446 - 1/13 - delete at end of file

Ill: net page formore enous

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Input Set : A:\PTO.AMC.txt
                     Output Set: N:\CRF3\03222001\1402093.raw
      3 <110> APPLICANT: Suntory Limited
      5 <120> TITLE OF INVENTION: Process for producing peptides using a
             helper peptide
      8 <130> FILE REFERENCE: F962
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/402,093
C--> 10 <141> CURRENT FILING DATE: 1999-09-29
     10 <150> PRIOR APPLICATION NUMBER: JP 10-032272
     11 <151> PRIOR FILING DATE: 1998-01-30
     13 <160> NUMBER OF SEQ ID NOS: 24
     15 <210> SEQ ID NO: 1
     16 <211> LENGTH: 4
     17 <212> TYPE: PRT
     18 <213> ORGANISM: Artificial Sequence
     20 <220> FEATURE:
     21 <223> OTHER INFORMATION: Amino acid sequence adjacent to a site cleaved by
     22
              enterokinase
     24 <400> SEQUENCE: 1
     25 Asp Asp Asp Lys
     26 1
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     30 <212> TYPE: PRT
     31 <213> ORGANISM: Artificial Sequence
W--> 32 <220> FEATURE:
     33 <223> OTHER INFORMATION: Amino acid sequence adjacent to a site cleaved by
             blood coagulation Factor Xa
W--> 35 <400> SEQUENCE: 2
     36 Ile Glu Gly Arg
     37
        1
     40 <210> SEQ ID NO: 3
     41 <211> LENGTH: 7
     42 <212> TYPE: PRT
     43 <213> ORGANISM: Artificial Sequence
    45 <220> FEATURE:
    46 <223> OTHER INFORMATION: Amino acid sequence containing a site cleaved by
    47
             renin
     49 <400> SEQUENCE: 3
     50 Pro Phe His Leu Leu Val Tyr
    51. 1
    53 <210> SEQ ID NO: 4
    54 <211> LENGTH: 6
    55 <212> TYPE: PRT
                                                   -) see item 12 on Eva Summary
Sheet
     56 <213> ORGANISM: Artificial Sequence
     58 <220> FEATURE:
    59 <223> OTHER INFORMATION:
    61 <400> SEQUENCE: 4
    62 Val Asp Asp Asp Lys
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DATE: 03/22/2001 TIME: 10:04:17

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/402,093

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/402,093

DATE: 03/22/2001. TIME: 09:36:29

Input Set : A:\F962 SEQUENCE.txt

Output Set: N:\CRF3\03222001\1402093.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No L:10 H:271 C: Current Fiting Date differs, Replaced Current Filing Date L:29 M:283 W: Missing Blank Line separator, <220> field identifier L:29 M:256 W: Invalid Numeric Header Field, <220> has non-blank data L:31 M:282 W: Numeric Field Identifier Missing, <211> is required. L:31 M:282 W: Numeric Field Identifier Missing, <212> is required. L:31 M:282 W: Numeric Field Identifier Missing, <212> is required. L:31 M:283 W: Missing Blank Line separator, <400> field identifier L:436 M:333 E: Wrong sequence grouping. Amino acids not in groups! L:446 M:332 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 L:444 M:333 E: Wrong sequence grouping, Amino acids not in groups! M:332 Repeated in SeqNov24 L:446 M:333 E: Wrong sequence grouping, Amino acids not in groups!